A146 Forensic Mitochondrial DNA Analysis of Human Hairs After Exposure to Radiation

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The goal of this presentation is to inform of the effects that radiation type and dosage have on Mitochondrial DNA (mtDNA) analysis of human hairs, allowing one to judge in which situations hair evidence is likely to remain useful for mtDNA analysis, and, therefore, should be collected.

This presentation will impact the forensic science community by understanding how the effects of radiation on the mtDNA analysis of hairs will prevent unnecessary radiation exposure to the individuals that would collect the hair evidence. This presentation will give decision makers more data to help determine whether or not the exposure of evidence to certain levels and types of radiation justifies the potential health risk for the evidence to be collected.

The objective of this presentation is to inform the forensic community of the effects that radiation type and dosage have on Mitochondrial DNA (mtDNA) analysis of human hairs. This will allow one to evaluate in which situations hair evidence is likely to remain useful for mtDNA analysis and; therefore, should be collected. In this way, knowing the effects of radiation on the mtDNA analysis of hairs will prevent unnecessary radiation exposure to the individuals that would collect the hair evidence.

Studies have shown the effects of DNA recovery from gamma irradiated human blood and paper[1] and the effects on nuclear DNA profile analysis from gamma and alpha irradiation of human blood, bone, saliva, and a genomic standard.[2] Here human hairs were irradiated with varying levels of gamma, neutron, beta, and alpha radiation in an attempt to determine the effect of these exposures on mtDNA analysis.

The hair samples were exposed to various levels of the four different types of radiation at the Savannah River National Laboratory, South Carolina, in replicates of five hairs per treatment for each of three individuals. Radiation doses included gamma ($5x10^4$ – $9x10^8$ rad), beta ($5x10^1$ – $1x10^3$ rad), alpha ($5x10^7$ - $5x10^{11}$ MeV), and neutron ($1x10^{10}$ – $1x10^{13}/cm^2$). Hair samples exposed to the highest radiation doses within each radiation treatment were initially extracted, mtDNA hypervariable regions I and II were amplified, the regions cycle-sequenced and sequenced, and finally the data were analyzed. These procedures followed the FBI Laboratory Mitochondrial DNA Unit Mitochondrial DNA Analysis Protocol (revision 5), with one exception: only one HL60 positive control sample and one negative control sample were amplified and analyzed per mtDNA region, per radiation treatment. When extraction, amplification, or sequencing of mtDNA was not successful within an irradiated sample dose, analysis of additional hairs was attempted. If mtDNA from the additional hairs was not successfully extracted, amplified, and sequenced, then hairs exposed to the next lower dose of that radiation type were analyzed. DNA extraction was successfully attempted on all hairs exposed to the highest dose of each radiation type, with the exception of the gamma $9x10^8$ rad treatment. Hairs exposed to that level of gamma radiation were physically degraded and not suitable for extraction.

Once mtDNA sequences were obtained from irradiated hairs, the mtDNA sequences were compared to mtDNA sequences from nonirradiated hairs from the same individual. These comparison hairs were subject to the same conditions as the irradiated hairs minus the radiation exposure (brought from the FBI laboratory to the Savannah River National Laboratory and back at the same time and stored in the same conditions).

DNA amplification was successful for all hairs exposed to each radiation treatment that were suitable for extraction, with the exception of the $1x10^6$ rad gamma radiation treatment. Only one of five hairs exposed to the $1x10^6$ rad level of gamma radiation produced extracted DNA with successful mtDNA amplification. All hairs exposed to the next highest level of gamma radiation ($1x10^5$), that were extracted for DNA, produced mtDNA amplification products.

Sequences were obtained for all hairs that produced acceptable mtDNA amplification products. These sequences from exposed hairs were identical in type to non-exposed hairs from the same individual. In addition, sequence quality of non-exposed hairs and exposed hairs was comparable, and independent of radiation type.

Collection of hair evidence near or directly from sources of radiation can be hazardous to the individual collector. For example, a gamma dose of 25-40 kGy ($2.5x10^6$-$4x10^6$ rad) is typical for food and pharmaceutical sterilization, and for humans, a whole-body dose of only 0.6-1 Gy (60-100 rad) is fatal almost 100% of the time (the radiation levels in the worst areas of the Chernobyl site are estimated at 200 Gy/hr or $2x10^4$ rad/hr). This study and presentation will give decision makers more data to help determine whether or not the exposure of evidence to certain levels and types of radiation justifies the potential health risk for the evidence to be collected.

References:

1. Hoile R, Banos C, Colella M, Walsh S, Roux C. Gamma irradiation as a biological decontaminant and its effect on common fingermark detection techniques and DNA profiling. J Forensic Sci 2010;55(1):171-7.
2. Abbondante S. The effect of radioactive materials on Forensic DNA evidence: procedures and interpretation [dissertation]. Canberra, Australia: University of Canberra. Canberra, Australia, 2009.

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